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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/647,067	09/25/2000	Aaron J. W. Hsueh	EL539 356 27	3881

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EXAMINER
BUNNER, BRIDGET E

ART UNIT	PAPER NUMBER
1647	

DATE MAILED: 04/23/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/647,067	HSUEH ET AL.	
	Examiner	Art Unit	
	Bridget E. Bunner	1647	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 February 2003* .

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,2,4 and 7-18* is/are pending in the application.

4a) Of the above claim(s) *12-17* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-2, 4, 7-11, and 18* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) *1,2,4 and 7-18* are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other:

DETAILED ACTION

Status of Application, Amendments and/or Claims

The amendment of 07 February 2003 (Paper No. 14) has been entered in full. Claims 1, 2, 4, 7, 10-11, and 18 are amended and claims 3, 5, 6 are cancelled.

This application contains claims 12-17 drawn to an invention nonelected without traverse in Paper No. 11 (12 August 2002). A complete reply to the final rejection must include cancellation of nonelected claims or other appropriate action (37 CFR 1.144) See MPEP § 821.01.

The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

Claims 1-2, 4, 7-11 and 18 are under consideration in the instant application.

Withdrawn Objections and/or Rejections

1. The objections to the specification at pg 3 of the previous Office Action (Paper No. 13,06 November 2002) are *withdrawn* in view of the submitted abstract and amended specification (Paper No. 14, 07 February 2003).

2. The rejection of claim 18 under 35 U.S.C. § 112, first paragraph (enablement) as set forth at pg 10-11 of the previous Office Action (Paper No. 13, 06 November 2002) is *withdrawn in part* in view of Applicant's persuasive arguments (Paper No. 14, 07 February 2003). Please see section below on 35 U.S.C. § 112, first paragraph.

3. The rejection of claims 1-11 and 18 under 35 U.S.C. § 112, second paragraph as set forth at pg 13-15 of the previous Office Action (Paper No. 13, 06 November 2002) is *withdrawn in*

part in view of the amended and cancelled claims. Please see section below on 35 U.S.C. § 112, second paragraph.

4. The rejection of claim 5-6 under 35 U.S.C. § 102(b) as set forth at pg 15-16 of the previous Office Action is *withdrawn* in view of the cancelled claims (Paper No. 14, 07 February 2003).

Sequence Compliance

5. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). **Specifically, the sequences disclosed in Figures 5 and 6 are not accompanied by the required reference to the relevant sequence identifiers.** This application fails to comply with the requirements of 37 CFR 1.821 through 1.825. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825). The basis for this objection is set forth at pg 2 of the previous Office Action (Paper No. 13, 06 November 2002).

Although Applicant has submitted a substitute sequence listing (paper and CRF), the Brief Description of Drawings at pg 2 of the specification does not identify the sequence identifiers (SEQ ID NOs:) associated with the sequences listed in Figures 5 and 6. It is suggested to Applicant that the specification at pg 2 be amended to include the SEQ ID NOs of the sequences in Figures 5 and 6.

Claim Objections

6. Claims 1-2, 4, and 7 are objected to because of the following informalities:

Claims 1-2, 4, and 7 recite non-elected groups (not related to LGR7). The basis for this rejection is set forth at pg 3 of the previous Office Action (Paper No. 13, 06 November 2002).

Applicant's arguments (Paper No. 14, 07 February 2003), as they pertain to the rejections have been fully considered but are not deemed to be persuasive for the following reasons.

At page 5 of the Response, Applicant states that the claims are amended to refer to an LGR7 protein. Applicant argues that claims 4 and 7 are amended to refer to SEQ ID NOs: 5 or 7. Applicant asserts that both SEQ ID NOs: 5 and 7 are LGR7 polynucleotides, encoding LGR7 polypeptides having the amino acid sequence set forth in SEQ ID NOs: 6 and 8, respectively.

Applicant's arguments have been fully considered but are not found to be persuasive. Specifically, in the Restriction of 11 March 2002 (Paper No. 7), Applicant was required to elect one nucleic acid group and one polypeptide group for examination (pg 3). In the Response of 12 August 2002 (Paper No. 13), Applicant elected LGR7 of SEQ ID NO: 7 for examination. Since Applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election was treated as an election without traverse. Therefore, the claims were examined to the extent that they read on LGR7 of the nucleic acid sequence of SEQ ID NO: 7 and of the amino acid sequence of SEQ ID NO: 8. The nucleic acid sequences of SEQ ID NOs: 5 and 7 are different lengths, composed of different nucleic acids, and are structurally and functionally unrelated to each other. Furthermore, the amino acid sequences of SEQ ID NOs: 6 and 8 are different lengths, composed of different amino acids, and are structurally and functionally unrelated to each other. It is suggested that claims 1-2, 4, and 7 are amended to remove reference to SEQ ID NOs: 5 and 6.

Appropriate correction is required.

Claim Rejections - 35 USC § 101 and § 112, first paragraph

7. Claims 1-2, 4, 7-11, and 18 are rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a credible, specific and substantial asserted utility or a well established utility. Novel biological molecules lack well established utility and must undergo extensive experimentation. The basis for this rejection is set forth at pg 3-8 of the previous Office Action (Paper No. 13, 06 November 2002).

Claims 1-2, 4, 7-11, and 18 are directed to an isolated nucleic acid encoding a mammalian LGR7 protein, wherein the LGR7 protein comprises an amino acid sequence having at least 80% amino acid sequence identity to the sequence set forth in SEQ ID NO: 8. The claims also recite an isolated nucleic acid wherein the nucleotide sequence has the sequence of SEQ ID NO: 7. The claims recite an expression cassette, a host cell, and a method of producing a mammalian protein. The claims are also directed to a purified polypeptide composition comprising a mammalian LGR7 protein or fragment thereof, wherein the LGR7 protein is at least about 80% and wherein the LGR7 protein comprises an amino acid sequence having at least 80% amino acid sequence identity to the sequence set forth in SEQ ID NO: 8. The claims are directed to a method of screening a sample for the presence of a ligand for a LGR7 receptor.

Applicant's arguments (Paper No. 14, 07 February 2003), as they pertain to the rejections have been fully considered but are not deemed to be persuasive for the following reasons.

(i) Applicant asserts that the specification teaches the LGR7 polypeptide functions as a G protein coupled receptor (GPCR). Applicant also argues that the claimed polynucleotides are useful for producing LGR7 polypeptides, which polypeptides are useful for the identification of a ligand, for screening for agonists and antagonists, and for the generation of functional binding

proteins for the neutralization of the action of an endogenous ligand. Applicant contends that the specification therefore provides a number of credible, specific, and substantial utilities for the claimed polynucleotides.

Applicant's arguments have been fully considered but are not found to be persuasive. The asserted utilities put forth by the Applicant and the specification of the instant application are credible, but not specific or substantial. The asserted utilities of identification of a ligand, screening for agonists and antagonists, and generation of functional binding proteins can be performed with any polypeptide. The specification also discloses nothing specific or substantial about the ligands, agonists/antagonists, and binding proteins that are identified by these methods. Since these asserted utilities are also not present in mature form, so that they could be readily used in a real world sense, the asserted utilities are not substantial.

(ii) Applicant asserts that the instant claims are supported by a credible, specific, and substantial utility as demonstrated in Hsu et al. (Science 295: 671-674, 2002). Applicant states that Hsu et al. teach that LGR7 binds relaxin, and that relaxin activates adenylate cyclase through G_s proteins upon relaxin binding. Applicant indicates that Hsu et al. demonstrate that LGR7 (1) functions as a GPCR; (2) is useful for the identification of a ligand for LGR7; (3) us useful for screening agonists and antagonists; and (4) is useful for the generation of functional binding proteins that neutralize the action of endogenous ligands.

Applicant's arguments have been fully considered but are not found to be persuasive. Although Hsu et al. demonstrate that the LGR7 protein of SEQ ID NO: 8 could be utilized to identify relaxin, the specification as originally filed does not suggest this utility. The Examiner acknowledges that the asserted utility of LGR7 being a receptor (specifically a GPCR) is

credible. However, the assertion that the orphan LGR7 receptor has utility as a GPCR is not specific or substantial. The asserted utilities for the identification of a ligand, screening for agonists/antagonists, and screening for binding proteins are also acknowledged as being credible, but not specific or substantial. The only credible, specific and substantial utility shown by Hsu et al. is that the LGR7 receptor 's ligand is relaxin. However, this utility is not asserted in the specification as originally filed.

8. Claims 1-2, 4, 7-11, and 18 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention. The basis for this rejection is set forth at pg 8-10 of the previous Office Action (Paper No. 13, 06 November 2002).

Applicant asserts that as discussed above, the specification provides a number of specific and substantial asserted utilities.

Applicant's arguments have been fully considered but are not found to be persuasive. Specifically, since Applicant has not provided evidence to demonstrate that the LGR7 polynucleotide and polypeptide have a specific and substantial asserted utility or a well established utility, one skilled in the art would not know how to use the claimed invention.

9. Furthermore, claims 1-2, 4, 8-11, and 18 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly

connected, to make and/or use the invention. The basis for this rejection is set forth for originally filed claims 5-6 and 11 at pg 8-10 of the previous Office Action (Paper No. 13, 06 November 2002).

Applicant's arguments (Paper No. 14, 07 February 2003), as they pertain to the rejections have been fully considered but are not deemed to be persuasive for the following reasons.

Applicant states that claims 5-6 are cancelled without prejudice, thereby rendering the rejection for these claims moot. Applicant also asserts that the specification discusses various polypeptide fragments of LGR7 and their uses (pg 9-11). Applicant indicates the specification teaches that the extracellular domain of LGR7 is useful in the neutralization of the action of endogenous ligands. Applicant argues that Hsu et al. (Molec Endocrinol 14: 1257-1271, 2000) demonstrates that a soluble extracellular domain of LGR7 functions as antagonist to LGR7, neutralizing the action of the ligand, relaxin. Applicant contends that those of skill in the art, given the guidance in the specification, would know which fragments of LGR7 would be expected to function as discussed in the specification. Applicant also submits that based on the alignments provided in Figure 6, those skilled in the art could readily determine, without experimentation, those amino acids of LGR7 that could be altered without changing the function of LGR7. Hsu et al. teach that based on an alignment of the LGR7 amino acid sequence with those of other hormone-binding GPCR, point mutations were made in LGR7 that affected its function as a GPCR.

Applicant's arguments have been fully considered but are not found to be persuasive. It is noted that claims 1-2, 4, 8-11, and 18 have been amended to recite 80% identity language. The specification teaches that "LGR7 polypeptide/protein is meant [to be] an amino acid

sequence encoded by an open reading frame of LGR7 genes, including the full-length native polypeptide and fragments thereof, particularly biologically active fragments corresponding to functional domains..." (pg 9, lines 22-25). The specification also discloses that the sequence changes may be substitutions, insertions, deletions, or a combination thereof (pg 8, lines 17-18). However, the specification also does not teach LGR7 nucleic acid variants or polypeptide variants. Further, the specification does not teach any functional or structural characteristics of the variants or fragments of the nucleic acid of SEQ ID NO: 7 or the polypeptide of SEQ ID NO: 8. The references in the previous Office Action (Paper No. 13, 06 November 2002) were cited to emphasize that the problem of predicting protein and DNA structure from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein and DNA is extremely complex. Certain positions in the amino acid sequence are critical to the protein's structure/function relationship, e.g. such as various sites or regions directly involved in binding, activity, and in providing the correct three-dimensional spatial orientation of binding and active sites. These regions can tolerate only relatively conservative substitutions or no substitutions. Related literature, such as Spiegel (Annual Rev. Physiol. 58:143-170, 1995) and Pauwels et al. (Molec. Neurobiol. 17(1-3): 109-135, 1998) discuss gain-of-function and loss-of-function mutations in G protein-coupled receptors that cause a wide spectrum of hereditary and somatic disorders and diseases. For example, the ***single*** mutation of a lysine residue to a glutamate residue at position 296 in the rhodopsin receptor results in constitutive activation of that receptor and autosomal dominant retinitis pigmentosa (see Pauwels et al., pg 122, table 3). Applicant has provided little or no guidance beyond the mere presentation of sequence data to enable one or ordinary skill in the art to determine, without undue experimentation, the positions

in the LGR7 protein and DNA which are tolerant to change and the nature and extent of changes that can be made in these positions.

Additionally, based on the alignments provided in Figure 6, those of skill in the art would not be able to determine, without undue experimentation, the amino acids of LGR7 that could be altered without changing the function of LGR7. Specifically, the sequences listed in Figure 6 are not for LGR7, but rather LGR4 and LGR5. The specification also does not disclose the location of LGR7's transmembrane domains, extracellular domain, ectodomain, etc. Applicant's assertion that the skilled artisan could identify and mutate amino acid residues of LGR7 based on alignments with other hormone-binding GPCRs cannot be accepted in the absence of supporting evidence, because the relevant literature reports examples of polypeptide families wherein individual members have distinct, and sometimes even opposite, biological activities. For example, Tischer et al. (U.S. Patent 5,194,596) establishes that VEGF (a member of the PDGF, or platelet-derived growth factor, family) is mitogenic for vascular endothelial cells but not for vascular smooth muscle cells, which is opposite to the mitogenic activity of naturally occurring PDGF which is mitogenic for vascular smooth muscle cells but not for vascular endothelial cells (column 2, line 46 to column 3, line 2). The differences between PDGF and VEGF are also seen *in vivo*, wherein endothelial-pericyte associations in the eye are disrupted by intraocular administration of PDGF but accelerated by intraocular administration of VEGF (Benjamin et al., 1998, Development 125:1591-1598; see Abstract and pp. 1594-1596). In the transforming growth factor (TGF) family, Vukicevic et al. (1996, PNAS USA 93:9021-9026) disclose that OP-1, a member of the TGF-β family of proteins, has the ability to induce metanephrogenesis, whereas closely related TGF-β family members BMP-2 and TGF-β1 had no effect on

metanephrogenesis under identical conditions (p. 9023, paragraph bridging columns 1-2). See also Massague, who reviews other members of the TGF-β family (1987, Cell 49:437-8, esp. p. 438, column 1, second full paragraph to the end). Similarly, PTH and PTHrP are two structurally closely related proteins which can have opposite effects on bone resorption (Pilbeam et al., 1993, Bone 14:717-720; see p. 717, second paragraph of Introduction). Finally, Kopchick et al. (U.S. Patent 5,350,836) disclose several antagonists of vertebrate growth hormone that differ from naturally occurring growth hormone by a single amino acid (column 2, lines 37-48).

Generally, the art acknowledges that function cannot be predicted based solely on structural similarity to a protein found in the sequence databases. For example, Skolnick et al. (2000, Trends in Biotech. 18:34-39) state that knowing the protein structure by itself is insufficient to annotate a number of functional classes, and is also insufficient for annotating the specific details of protein function (see Box 2, p. 36). Similarly, Bork (2000, Genome Research 10:398-400) states that the error rate of functional annotations in the sequence database is considerable, making it even more difficult to infer correct function from a structural comparison of a new sequence with a sequence database (see especially p. 399). Such concerns are also echoed by Doerks et al. (1998, Trends in Genetics 14:248-250) who state that (1) functional information is only partially annotated in the database, ignoring multi functionality, resulting in underpredictions of functionality of a new protein and (2) overpredictions of functionality occur because structural similarity often does not necessarily coincide with functional similarity. Smith et al. (1997, Nature Biotechnology 15:1222-1223) remark that there are numerous cases in which proteins having very different functions share structural similarity due to evolution from a common ancestral gene. Brenner (1999, Trends in Genetics 15:132-133) argues that accurate

inference of function from homology must be a difficult problem since, assuming there are only about 1000 major gene superfamilies in nature, then most homologs must have different molecular and cellular functions. Finally, Bork et al. (1996, Trends in Genetics 12:425-427) add that the software robots that assign functions to new proteins often assign a function to a whole new protein based on structural similarity of a small domain of the new protein to a small domain of a known protein. Such questionable interpretations are written into the sequence database and are then considered facts.

Proper analysis of the Wands factors was performed in the previous Office Action. Due to the large quantity of experimentation necessary to generate the infinite number of derivatives recited in the claims and possibly screen same for activity, the lack of direction/guidance presented in the specification regarding which structural features are required in order to provide activity, the absence of working examples directed to same, the complex nature of the invention, the state of the prior art which establishes the unpredictability of the effects of mutation on protein structure and function and that biological activity cannot be predicted based on structural similarity, and the breadth of the claims which fail to recite any structural or functional limitations and also embrace a broad class of structural fragments and variants, undue experimentation would be required of the skilled artisan to make and/or use the claimed invention in its full scope.

10. Claims 1-2, 4, 8-11, and 18 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the

application was filed, had possession of the claimed invention. The basis for this rejection is set forth for originally filed claims 5-6 and 11 at pg 11-13 of the previous Office Action (Paper No. 13, 06 November 2002).

Claims 1-2, 4, 8-11, and 18 are directed to an isolated nucleic acid encoding a mammalian LGR7 protein, wherein the LGR7 protein comprises an amino acid sequence having at least 80% amino acid sequence identity to the sequence set forth in SEQ ID NO: 8. The claims are also directed to a purified polypeptide composition comprising a mammalian LGR7 protein or fragment thereof, wherein the LGR7 protein is at least about 80% and wherein the LGR7 protein comprises an amino acid sequence having at least 80% amino acid sequence identity to the sequence set forth in SEQ ID NO: 8.

Applicant's arguments (Paper No. 14, 07 February 2003), as they pertain to the rejections have been fully considered but are not deemed to be persuasive for the following reasons.

Applicant asserts that claims 5-6 are cancelled without prejudice, thereby rendering this rejection of these claims moot. Applicant also contends that the specification provides the nucleotide and amino acid sequences of at least two LGR7 polypeptides. Applicant states that the specification teaches the LGR7 polypeptides are encoded by splice variants and that the specification provides guidance for various fragments of LGR7 polypeptides and their uses.

Applicant's arguments have been fully considered but are not found to be persuasive. Applicant has not provided evidence to demonstrate that the skilled artisan would be able to envision the detailed structure of the infinite number of polynucleotides recited in the claims. The description of two LGR7 polynucleotides and polypeptides in the specification of the instant application is not a representative number of embodiments to support the description of an entire

genus of functionally equivalent polynucleotides and polypeptides which incorporate all mutants, derivatives, and fragments having at least 80% identity to the nucleic acid sequences of SEQ ID NO: 7 and the amino acid sequences of SEQ ID NO: 8. Therefore, only an isolated nucleic acid molecule consisting of the nucleotide sequence of SEQ ID NO: 7 and an amino acid sequence of SEQ ID NO: 8, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Furthermore, the broad brush discussion of making or screening for fragments does not constitute a disclosure of a representative number of members. No such fragments were made or shown to have activity. Only one member, LGR7 of SEQ ID NO: 6 and 8, was disclosed. The specification's general discussion of making and screening for variants constitutes an invitation to experiment by trial and error. Such does not constitute an adequate written description for the claimed derivatives.

35 USC § 112, second paragraph

11. Claim 7 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The basis for this rejection is set forth for originally filed claims 1-11 and 18 at pg 13-15 of the previous Office Action (Paper No. 13, 06 November 2002).

12. Regarding claim 7, the phrase "complementary sequence thereof" renders the claim indefinite because it is unclear whether "complementary sequence thereof" refers to the entire nucleic acid sequence complement or variants and fragments of the complement. The basis for this rejection is set forth for originally filed claims 4-7 at pg 14 of the previous Office Action (Paper No. 13, 06 November 2002).

Applicant's arguments (Paper No. 14, 07 February 2003), as they pertain to the rejections have been fully considered but are not deemed to be persuasive for the following reasons.

Applicant asserts at pg 9-10 of the Response that claims 5-6 are cancelled without prejudice, thereby rendering the rejection of these claims moot. Applicant's arguments have been fully considered but are not found to be persuasive because claim 7 still recites "complementary sequence thereof".

Conclusion

No claims are allowable.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Bridget E. Bunner whose telephone number is (703) 305-7148. The examiner can normally be reached on 8:30-5:30 M-F.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Kunz can be reached on (703) 308-4623. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 872-9306 for regular communications and (703) 872-9307 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 872-9305.

Elizabeth C. Kemmerer

BEB
Art Unit 1647
April 10, 2003

ELIZABETH KEMMERER
PRIMARY EXAMINER